

Application No. 09/823,649

Appendix D

(6 pages)

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entry O52225

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Entry information

Entry name DPO1_THEFI
Primary accession number O52225
Secondary accession numbers None
Integrated into Swiss-Prot on December 15, 1998
Sequence was last modified on June 1, 1998 (Sequence version 1)
Annotations were last modified on March 7, 2006 (Entry version 38)

Name and origin of the protein

Protein name DNA polymerase I, thermostable
Synonyms EC 2.7.7.7
Gene name TFI polymerase 1
Synonyms: polA

From Thermus filiformis [TaxID: 276]
Taxonomy Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Thermus.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

PubMed=9509419 [NCBI, ExPASy, EBI, Israel, Japan]

Jung S.E., Choi J.J., Kim H.K., Kwon S.-T.;

"Cloning and analysis of the DNA polymerase-encoding gene from *Thermus filiformis*.";

Mol. Cells 7:769-776(1997).

Comments

- **FUNCTION:** Has 5'-to-3' exonuclease activity and no 3'-to-5' exonuclease activity.
- **CATALYTIC ACTIVITY:** Deoxynucleoside triphosphate + DNA(n) = diphosphate + DNA(n+1).
- **BIOPHYSICOCHEMICAL PROPERTIES:**
 - Temperature dependence:* Thermostable;
- **SIMILARITY:** Belongs to the DNA polymerase type-A family.
- **SIMILARITY:** Contains 1 5'-3' exonuclease domain.

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Cross-references

Sequence databases

EMBL AF030320; AAC46079.1; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases

HSSP P19821; 1TAQ. [HSSP ENTRY / PDB]

ModBase Q52225.

Protein-protein interaction databases

DIP Q52225.

2D gel databases

SWISS-2DPAGE Get region on 2D PAGE.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Family and domain databases

IPR002421; 5_3_exonuclease.

InterPro IPR001098; DNA_pol.

IPR002298; DNA_poll.

IPR000513; Exo_N_I.

IPR008918; HhH2.
 IPR012337; RNaseH_fold.
 Graphical view of domain structure.
 PF01367; 5_3_exonuc; 1.
 PF02739; 5_3_exonuc_N; 1.
 PF00476; DNA_pol_A; 1.
 Pfam graphical view of domain structure.
 PRINTS
 PR00868; DNAPOLI.
 SM00475; 53EXOC; 1.
 SM00279; HhH2; 1.
 SMART
 SM00482; POLAc; 1.
 SMART graphical view of domain structure.
 TIGRFAMs
 TIGR00593; pola; 1.
 PROSITE
 PS00447; DNA_POLYMERASE_A; 1.
 ProDom
 [Domain structure / List of seq. sharing at least 1 domain]
 BLOCKS
 O52225.

Other

ProtoNet
 O52225.

UniRef
 View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

DNA damage; DNA repair; DNA replication; DNA-binding; DNA-directed DNA polymerase; Nucleotidyltransferase; Transferase.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FeatId
CHAIN	1	833	833	DNA polymerase I, thermostable. PRO_0000101260	
REGION	412	833	422	Polymerase (By similarity).	

Sequence information

Length: 833 AA [This is the length of the unprocessed precursor]
 Molecular weight: 93891 Da [This is the MW of the unprocessed precursor]
 CRC64: 51BF8B0417EEFC4D [This is a checksum on the sequence]

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RMS Patent Department

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10	20	30	40	50	60
MTPLFDLEEP	PKRVLLVDGH	HLAYRTFYAL	SLTTSRGEFV	QMVYGFARSL	LKALKEDGQA
70	80	90	100	110	120
VVVVFDKAP	SFRHEAYEAY	KAGRAPTPE	FPRQLALVKR	LVDLLGLVRL	EAPGYEADDV
130	140	150	160	170	180
LGTLAKKAER	EGMEVRILT	DRDFFQLLSE	KVSULLPDGT	LVTPKDVQEK	YGVPPERWVD
190	200	210	220	230	240
FRALTGDRSD	NIPGVAGIGE	KTALRLLAEW	GSVENLLKNL	DRVKPDLSRR	KIEAHLEDLH
250	260	270	280	290	300
LSLDLARIRT	DLPLEVDEKA	LRRRTPDLEG	LRAFLEELEF	GSLLEHEFGLL	GGEKPREEAP
310	320	330	340	350	360
WPPPEGAFVG	FLLSRKEPMW	AELLALAAAS	EGRVHRATSP	VEALADLKEA	RGFLAKDLAV
370	380	390	400	410	420
LALREGVALD	PTDDPLLVA	LLDPANTHPE	GVARRYGGEF	TEDAAERALL	SERLFQNLFP
430	440	450	460	470	480
RLSEKLLWL	YQEVERPLSRV	LAHMEARGVR	LDVPLLEALS	FELLEKEMERL	EGEVFRLAGH
490	500	510	520	530	540
PFNLNSRDQL	ERVLFDLGL	TPVGRTEKTG	KRSTAQGALE	ALRGAHPIVE	LILQYRELSK
550	560	570	580	590	600
LKSTYLDPLP	RLVHPRTGRL	HTRFNQTATA	TGRLSSSDPN	LQNIPTVTP	LQIRKAFVA
610	620	630	640	650	660
EEGWLLAAD	YSQIELRVLA	HLSGDENLKR	VFREGKDIHT	ETAAMFGLD	PALVDPKMR
670	680	690	700	710	720

AAKTVNFGVL YGMSAHLRSQ ELGIDYKEAE AFIERVFQSF PKVRAWIERT LEEGRTRGYV
 730 740 750 760 770 780
 ETLFGRRRYV PDLASRVRSV REAAERMAFN MPVQGTAAADL MKIAMVKLFP RLKPLGAHLL
 790 800 810 820 830
 LQVHDELVL VPEDRAEAK ALVKEVMENA YPLDVPLEVE VGVGRDNL EA KQD

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BLAST

BLAST submission on ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw,
PeptideMass, PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-MODEL



NPSA Sequence analysis tools



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Feature aligner

Selected features of [O52225](#) (DPO1_THERF) DNA polymerase I, thermostable (EC 2.7.7.7) (TFI polymerase 1) [Thermus filiformis].

Key Position Length Description

☐ CHAIN 1-833 833

DNA polymerase I, thermostable

MTPLFDEEP PKRVLLVDGH HLAYRTFYAL SLTTSRGEVP QMVYGFARSL LKALKEDGQA VVVVFDKAP
SFRHEAYEAY KAGRPTPED FPRQLALVKR LVDLLGLVRL EAPGYEADVV LGTLAKAER EGMVVRILTQ
DRDFFQLLSE RVSLLPDGT LVTPKDVQEK YGVPERWVD FRALTGDRSD NIPGVAGIGE KTAIRLLAEW
GSVENLLKNL DRVKPDSLRR KIEAHLEDLH LSLDLARIT DPLFVDFFKA LRRTPDLEG LRAFLEELEF
GSLHEFGLL GGEKPREEP WPPPEGAFVG FLRSKEPMW AELLALAAAS EGRVHRATSP VEAALDLKEA
RGFLAKDLAV LALREGVALD PTDDLLVAV LLDPANTRPE GVARRYGGEF TEDAAERALL SBRLLFQNLFP
RLSEKLLWLY QEVERPLSRV LAHNEARGVR LDVPLLEALS FELKEMERL EGVFRLAGH PFNLSRDQL
ERVLFDLGL TPVGRTEKTG KRSTAQGALE ALRGHPIVE LILQVRELSK LKSTYLDPLP RLVPRTGRL
HTRFNQTATA TGRSSSDPN LQNIPTVPTPL QQRIRKAPVA EEWLLLAAD YSQIELRVLA HLSGDNLKR
VFREGKDIHT ETAAMFGLD PALVDPKMR AAKTVNFGVL YGMSAHRLSQ ELGIDYKEAE AFIERVFSF
PKVRAMTERT LREGTRGYV ETLFGRRYV PDLASRVRSV REAARMFEN MPVQGTADL MKIAMVKLFP
RLKPLGAHLL LQVHDELAVLE VPEDRAEEAK ALVKEVMENA YPLDVPLEVE VGVGRDWLEA KQD

☐ REGION 412-833 422

Polymerase (By similarity)

ERLFQNLFP LSEKLLWLYQ EVERPLSRVL AHNEARGVRL DVPLLEALSF ELEKEMERLE GEVRLAGHP
FNLSRDQLE RVLFDELGLT PVGRTEKTGK RSTAQGALEA LRGAHPIVE LILQVRELSK KSTYLDPLPR
LVHPRTGRLH TRFNQTATAT GRSSSDPNL QNIPTVPTPLG QRIRKAPVAE EEWLLLAADY SQIELRVLAH
LSGDNLKR VREGKDIHT ETAAMFGLD PALVDPKMR AAKTVNFGVL YGMSAHRLSQ ELGIDYKEAE
FIERYFSFP KVRAMTERT LREGTRGYV ETLFGRRYV PDLASRVRSV REAARMFEN MPVQGTADL MKIAMVKLFP
KIAMVKLFP LKPLGAHLL QVHDELAVLE VPEDRAEEAK ALVKEVMENA YPLDVPLEVE VGVGRDWLEA KQD

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